

## SEQUENCE LISTING

<110> Alan Brash  
Nathalie Tijet

<120> MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE  
LYASE AND USES THEREOF

<130> 06027.0002

<160> 56

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 10  
<212> PRT  
<213> Cucumis melo

<400> 1  
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1 5 10

<210> 2  
<211> 15  
<212> PRT  
<213> Cucumis melo

<400> 2  
Ile Leu Phe Asp Thr Ala Lys Val Glu Lys Arg Asn Ile Leu Asp  
1 5 10 15

<210> 3  
<211> 8  
<212> PRT  
<213> Cucumis melo

<400> 3  
Arg Leu Phe Leu Ser Phe Leu Ala  
1 5

<210> 4  
<211> 7  
<212> PRT  
<213> Cucumis melo

<400> 4  
Ser Ile Ser Asp Ser Met Ser  
1 5

<210> 5  
<211> 8  
<212> PRT

<213> Cucumis melo

<400> 5

Leu Leu Ser Asp Gly Thr Pro Asp

1

5

<210> 6

<211> 10

<212> PRT

<213> Cucumis melo

<400> 6

Ile Phe Ser Val Phe Glu Asp Leu Val Ile

1

5

10

<210> 7

<211> 481

<212> PRT

<213> Cucumis melo

<400> 7

Met	Ala	Thr	Pro	Ser	Ser	Ser	Ser	Pro	Glu	Leu	Pro	Leu	Lys	Pro	Ile
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Pro	Gly	Gly	Tyr	Gly	Phe	Pro	Phe	Leu	Gly	Pro	Ile	Lys	Asp	Arg	Tyr
			20					25				30			
Asp	Tyr	Phe	Tyr	Phe	Gln	Gly	Arg	Asp	Glu	Phe	Phe	Arg	Ser	Arg	Ile
		35					40					45			
Thr	Lys	Tyr	Asn	Ser	Thr	Val	Phe	Arg	Ala	Asn	Met	Pro	Pro	Gly	Pro
		50				55					60				
Phe	Ile	Ser	Ser	Asp	Ser	Arg	Val	Val	Val	Leu	Leu	Asp	Ala	Leu	Ser
				70						75				80	
Phe	Pro	Ile	Leu	Phe	Asp	Thr	Ala	Lys	Val	Glu	Lys	Arg	Asn	Ile	Leu
				85					90					95	
Asp	Gly	Thr	Tyr	Met	Pro	Ser	Leu	Ser	Phe	Thr	Gly	Asn	Ile	Arg	Thr
			100					105				110			
Cys	Ala	Tyr	Leu	Asp	Pro	Ser	Glu	Thr	Glu	His	Ser	Val	Leu	Lys	Arg
		115					120					125			
Leu	Phe	Leu	Ser	Phe	Leu	Ala	Ser	Arg	His	Asp	Arg	Phe	Ile	Pro	Leu
		130				135					140				
Phe	Arg	Ser	Ser	Leu	Ser	Glu	Met	Phe	Val	Lys	Leu	Glu	Asp	Lys	Leu
		145			150					155				160	
Ser	Glu	Lys	Lys	Lys	Ile	Ala	Asp	Phe	Asn	Ser	Ile	Ser	Asp	Ser	Met
			165				170						175		
Ser	Phe	Asp	Tyr	Val	Phe	Arg	Leu	Leu	Ser	Asp	Gly	Thr	Pro	Asp	Ser
		180					185					190			
Lys	Leu	Ala	Ala	Glu	Gly	Pro	Gly	Met	Phe	Asp	Leu	Trp	Leu	Val	Phe
		195				200					205				
Gln	Leu	Ala	Pro	Leu	Ala	Ser	Ile	Gly	Leu	Pro	Lys	Ile	Phe	Ser	Val
		210				215					220				
Phe	Glu	Asp	Leu	Val	Ile	His	Thr	Ile	Pro	Leu	Pro	Phe	Phe	Pro	Val
		225			230					235				240	
Lys	Ser	Gly	Tyr	Arg	Lys	Leu	Tyr	Glu	Ala	Phe	Tyr	Ser	Ser	Ser	Gly
			245						250					255	
Ser	Phe	Leu	Asp	Glu	Ala	Glu	Lys	Gln	Gly	Ile	Asp	Arg	Glu	Lys	Ala
		260					265					270			
Cys	His	Asn	Leu	Val	Phe	Leu	Ala	Gly	Phe	Asn	Ala	Tyr	Gly	Gly	Met
		275					280					285			

Lys Val Leu Phe Pro Thr Leu Leu Lys Trp Val Gly Thr Ala Gly Glu  
 290 295 300  
 Asp Leu His Arg Lys Leu Ala Glu Glu Val Arg Thr Thr Val Lys Glu  
 305 310 315 320  
 Glu Gly Gly Leu Thr Phe Ser Ala Leu Glu Lys Met Ser Leu Leu Lys  
 325 330 335  
 Ser Val Val Tyr Glu Ala Leu Arg Ile Glu Pro Pro Val Pro Phe Gln  
 340 345 350  
 Tyr Gly Lys Ala Lys Glu Asp Ile Val Ile Gln Ser His Asp Ser Ser  
 355 360 365  
 Phe Lys Ile Lys Lys Gly Glu Thr Ile Phe Gly Tyr Gln Pro Phe Ala  
 370 375 380  
 Thr Lys Asp Pro Lys Ile Phe Lys Asp Ser Glu Lys Phe Val Gly Asp  
 385 390 395 400  
 Arg Phe Val Gly Glu Glu Gly Glu Lys Leu Leu Lys Tyr Val Tyr Trp  
 405 410 415  
 Ser Asn Glu Arg Glu Thr Val Glu Pro Thr Ala Glu Asn Lys Gln Cys  
 420 425 430  
 Pro Gly Lys Asn Leu Val Val Leu Ile Gly Arg Ile Met Val Val Glu  
 435 440 445  
 Phe Phe Leu Arg Tyr Asp Thr Phe Thr Val Glu Val Ala Asp Leu Pro  
 450 455 460  
 Leu Gly Pro Ala Val Lys Phe Lys Ser Leu Thr Arg Ala Thr Asp Met  
 465 470 475 480  
 Val

&lt;210&gt; 8

&lt;211&gt; 1446

&lt;212&gt; DNA

&lt;213&gt; Cucumis melo

&lt;400&gt; 8

atggctactc cttcttctct ctccccgtgaa cttctcttca aaccaattcc cggtggctat 60  
 ggcttccccct tctctcggtcc catcaaaagac cgtttacgatt acttctattt ccaaggtaga 120  
 gcgaattctt tccgttcccg gattaccaaaa tacaactcca cgtcttcccg gcaccaactg 180  
 ccaccggggcc ccttcatttt ctccgattcc agagtcgttg tcttcttcga tgccctcagt 240  
 tttctctatct tcttccgacac agccaaagtc gagaaacgca acattctcga cggaactttac 300  
 atgcctctctc tgcctcttcc cggcaacatt cgcacctgtg cttattttgga cccatcgga 360  
 acagagcact ctgttctcaa acgctctctc ctctctcttc tgccttcccg ccatgacagg 420  
 ttcatccctc tgtttcgaag ctctgtgtct gagatgtttg ttaagcttga agataaactt 480  
 tccgagaaaa agaagatcgc tgatttcaac tcgatcagcg attcctatgct gtttgattat 540  
 gttttccggtt tactctccga tggaaacctt gattcgaaat tagctgctga gggacctgga 600  
 atgttgcgatc tgtggcttgt gtttcaactc gcccatgtg cttccatttg ccttcccaac 660  
 attttctctg tttttgaaga tctcgtcatt cacaccattc ccttgccttt cttcccgagt 720  
 aagagtgtgt acaggaagct ttatgaagcg ttttactcct cttctggtct atttctagac 780  
 gaagcagaga aacagggggat agacagggag aaagcatgtc acaatttagt gtttctcgct 840  
 ggattcaacg catacggggg aatgaaagtc ctttttccca ctttactgaa atgggtcggc 900  
 accgcgggcy aggatctcca ccggaaactc gccgaggaa gtcaggacaac cgtgaaggaa 960  
 gaagggggac tgactttctc cgccttggag aaaaatgagtc tgcgaagtc cgtcgtgtac 1020  
 gaagcactca ggtatcgaac gccggtgccc ttccagtagc ggaagcgaa ggaagtagatc 1080  
 gtgattcaga gcaacgattc tcttttcaag atcaaaaag gggagacgat ttttggttat 1140  
 cagcgcctttg ctactaaaga tccgaagatt ttaagagatt cggagaagtt cgtgggcat 1200  
 aggttcgttg gagaggaagg ggagaagcgt ttgaagtagt ttactgctc aaatgagcgg 1260  
 gagacagtag agccgacggc ggagaacaag cagtgctcgg ggaagaatct ggtggtgctg 1320  
 ataggtagga ttatggtggt ggaattcttc cttcgttatg atacgtttac cgtggaggctc 1380

gcagatttgc cgctgggtcc ggcagtgaa ttcaagtct taaccagagc aaccgatatg 1440  
gtttaa 1446

<210> 9  
<211> 60  
<212> PRT  
<213> Psidium Guava

<400> 9  
Gly Glu Leu Leu Cys Gly Tyr Gln Lys Val Val Met Thr Asp Pro Lys  
1 5 10 15  
Val Phe Asp Glu Pro Glu Ser Phe Asn Ser Asp Arg Phe Val Gln Asn  
20 25 30  
Ser Glu Leu Leu Asp Tyr Leu Tyr Trp Ser Asn Gly Pro Gln Thr Gly  
35 40 45  
Thr Pro Thr Glu Ser Asn Lys Gln Cys Ala Ala Lys  
50 55 60

<210> 10  
<211> 61  
<212> PRT  
<213> Banana

<400> 10  
Gly Glu Leu Leu Cys Gly Tyr Gln Pro Leu Val Met Arg Asp Pro Ala  
1 5 10 15  
Val Phe Asp Asp Pro Glu Thr Phe Ala Pro Glu Arg Phe Met Gly Ser  
20 25 30  
Gly Lys Glu Leu Leu Lys Tyr Val Phe Trp Ser Asn Gly Pro Glu Thr  
35 40 45  
Gly Thr Pro Thr Pro Ala Asn Lys Gln Cys Ala Ala Lys  
50 55 60

<210> 11  
<211> 62  
<212> PRT  
<213> Capsicum annum (green pepper)

<400> 11  
Gly Glu Leu Leu Cys Gly Tyr Gln Pro Leu Val Met Lys Asp Pro Lys  
1 5 10 15  
Val Phe Asp Glu Pro Glu Lys Phe Met Leu Glu Arg Phe Thr Lys Glu  
20 25 30  
Lys Gly Lys Glu Leu Leu Asn Tyr Leu Phe Trp Ser Asn Gly Pro Gln  
35 40 45  
Thr Gly Ser Pro Thr Glu Ser Asn Lys Gln Cys Ala Ala Lys  
50 55 60

<210> 12  
<211> 62  
<212> PRT  
<213> Arabidopsis

<400> 12  
Gly Glu Met Leu Tyr Gly Tyr Gln Pro Leu Ala Thr Arg Asp Pro Lys  
1 5 10 15

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Ile Phe Asp Arg Ala Asp Glu Phe Val Pro Glu Arg Phe Val Gly Glu
      20                25                30
Glu Gly Glu Lys Leu Leu Arg His Val Leu Trp Ser Asn Gly Pro Glu
      35                40                45
Thr Glu Thr Pro Thr Val Gly Asn Lys Gln Cys Ala Gly Lys
      50                55                60

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<210> 13  
 <211> 61  
 <212> PRT  
 <213> Flax

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<400> 13
Gly Glu Met Leu Phe Gly Tyr Gln Pro Phe Ala Thr Lys Asp Pro Lys
  1                5                10                15
Ile Phe Asp Arg Pro Glu Glu Phe Val Ala Asp Arg Phe Val Gly Glu
      20                25                30
Gly Val Lys Leu Met Glu Tyr Val Met Trp Ser Asn Gly Pro Glu Thr
      35                40                45
Glu Thr Pro Ser Val Ala Asn Lys Gln Cys Ala Gly Lys
      50                55                60

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<210> 14  
 <211> 61  
 <212> PRT  
 <213> Guayule

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<400> 14
Gly Glu Met Leu Phe Gly Tyr Gln Pro Phe Ala Thr Lys Asp Pro Lys
  1                5                10                15
Val Phe Asp Arg Pro Glu Glu Phe Val Ala Asp Arg Phe Val Gly Glu
      20                25                30
Gly Val Lys Leu Met Glu Tyr Val Trp Trp Ser Asn Gly Pro Glu Thr
      35                40                45
Glu Ser Pro Thr Val Glu Asn Lys Gln Cys Ala Gly Lys
      50                55                60

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<210> 15  
 <211> 487  
 <212> PRT  
 <213> Cucumis melo

<221> VARIANT  
 <222> (1)...(487)  
 <223> Xaa = Any Amino Acid

<221> misc\_feature  
 <222> (0)...(0)  
 <223> Accession No. AF081955

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<400> 15
Met Ala Thr Pro Ser Ser Ser Ser Pro Glu Leu Pro Leu Lys Pro Ile
  1                5                10                15
Pro Gly Gly Tyr Gly Phe Pro Phe Leu Gly Pro Ile Lys Asp Arg Tyr
      20                25                30

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Asp Tyr Phe Tyr Phe Gln Gly Arg Asp Glu Phe Phe Glu Arg Ser Arg  
 35 40 45  
 Ile Thr Lys Tyr Asn Ser Thr Val Phe Arg Ala Asn Met Pro Pro Gly  
 50 55 60  
 Pro Phe Ile Ser Ser Asp Ser Arg Val Val Val Leu Leu Asp Ala Leu  
 65 70 75 80  
 Ser Phe Pro Ile Leu Phe Asp Thr Ala Lys Val Glu Lys Arg Asn Ile  
 85 90 95  
 Leu Asp Gly Thr Tyr Met Pro Ser Leu Ser Phe Thr Gly Asn Ile Arg  
 100 105 110  
 Thr Cys Ala Tyr Leu Asp Pro Ser Glu Thr Glu His Ser Val Leu Lys  
 115 120 125  
 Arg Leu Phe Leu Ser Phe Leu Ala Ser Arg His Asp Arg Phe Ile Pro  
 130 135 140  
 Leu Phe Arg Ser Ser Leu Ser Glu Met Phe Val Lys Leu Glu Asp Lys  
 145 150 155 160  
 Leu Ser Glu Lys Lys Lys Ile Ala Asp Phe Asn Ser Ile Ser Asp Ser  
 165 170 175  
 Met Ser Phe Asp Tyr Val Phe Arg Leu Leu Ser Asp Gly Thr Pro Asp  
 180 185 190  
 Ser Lys Leu Ala Ala Glu Gly Pro Gly Met Phe Asp Leu Trp Leu Val  
 195 200 205  
 Phe Gln Leu Ala Pro Leu Ala Ser Ile Gly Leu Pro Lys Ile Phe Ser  
 210 215 220  
 Val Phe Glu Asp Leu Val Ile His Thr Ile Pro Leu Pro Phe Phe Pro  
 225 230 235 240  
 Val Lys Ser Gly Tyr Arg Lys Leu Tyr Glu Ala Phe Tyr Ser Ser Ser  
 245 250 255  
 Gly Ser Phe Leu Asp Glu Ala Glu Lys Gln Gly Ile Asp Arg Glu Lys  
 260 265 270  
 Ala Cys His Asn Leu Val Phe Leu Ala Gly Phe Asn Ala Tyr Gly Gly  
 275 280 285  
 Met Lys Val Leu Phe Pro Thr Leu Leu Lys Trp Val Gly Thr Ala Gly  
 290 295 300  
 Glu Asp Leu His Arg Lys Lys Leu Ala Glu Glu Val Arg Thr Thr Val Lys  
 305 310 315 320  
 Glu Glu Gly Gly Leu Thr Phe Ser Ala Leu Glu Lys Met Ser Leu Leu  
 325 330 335  
 Lys Ser Val Val Tyr Glu Ala Leu Arg Ile Glu Pro Pro Val Pro Phe  
 340 345 350  
 Gln Tyr Gly Lys Ala Lys Glu Asp Ile Val Ile Gln Ser His Asp Ser  
 355 360 365  
 Ser Phe Lys Ile Lys Lys Gly Glu Thr Ile Phe Gly Tyr Gln Pro Phe  
 370 375 380  
 Ala Thr Lys Asp Pro Lys Ile Phe Lys Asp Ser Glu Lys Phe Val Gly  
 385 390 395 400  
 Asp Arg Phe Val Gly Glu Glu Gly Glu Lys Leu Lys Tyr Val Tyr  
 405 410 415  
 Trp Ser Asn Glu Arg Glu Thr Val Glu Pro Thr Arg Xaa Asn Lys Gln  
 420 425 430  
 Cys Pro Gly Lys Asn Leu Val Val Leu Ile Gly Arg Ile Met Val Val  
 435 440 445  
 Glu Phe Phe Leu Arg Tyr Asp Thr Phe Thr Val Glu Val Ala Asp Leu  
 450 455 460  
 Pro Leu Gly Pro Ala Val Lys Phe Lys Ser Leu Thr Arg Ala Thr Asp  
 465 470 475 480

Met Leu Lys Leu Met Thr Asn  
485

<210> 16  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)...(23)  
<223> n = A,T,C or G  
y = C or T(U)

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 16  
ggtgagttgc tntgyggnta yca

23

<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)...(20)  
<223> n = A,T,C or G  
y = A,T,C or G

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 17  
ggtgagttgc tntgyggnta

20

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)...(20)  
<223> n = A,T,C or G  
y = C or T(U)

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 18  
tggtcnaayg gncrgagac

20

<210> 19  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)...(23)  
<223> n = A,T,C or G  
y = C or T(U)  
r = A or G

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 19  
tactggtcna ayggnccnsa rac

23

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)...(24)  
<223> n = A,T,C or G  
y = C or T(U)  
r = A or G

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 20  
aayaarcart gygngctaa ggac

24

<210> 21  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)...(21)  
<223> n = A,T,C or G  
y = C or T(U)  
r = A or G

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 21  
aarcartgyg cngctaagga c

21



<210> 22  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 22  
Gly Glu Leu Leu Cys Gly Tyr Gln  
1 5

<210> 23  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 23  
Gly Glu Leu Leu Cys Gly Tyr  
1 5

<210> 24  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 24  
Trp Ser Asn Gly Pro Glu Thr  
1 5

<210> 25  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 25  
Tyr Trp Ser Asn Gly Pro Glu Thr  
1 5

<210> 26  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> VARIANT  
<222> (1)... (8)  
<223> Xaa = Any Amino Acid  
  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 26  
Asn Lys Gln Cys Ala Ala Xaa Xaa  
1 5

<210> 27  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> VARIANT  
<222> (1)... (7)  
<223> Xaa = Any Amino Acid  
  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 27  
Lys Gln Cys Ala Ala Xaa Xaa  
1 5

<210> 28  
<211> 32  
<212> PRT  
<213> Cucumis melo

<400> 28  
Gly Glu Leu Leu Cys Gly Tyr Gln Pro Leu Val Met Arg Asp Pro Lys  
1 5 10 15  
Val Phe Asp Glu Pro Glu Ala Phe Asn Pro Asp Arg Phe Arg Gly Glu  
20 25 30

<210> 29  
<211> 32  
<212> PRT  
<213> Cucumis melo

<400> 29  
Gly Glu Leu Leu Cys Gly Tyr Gln Pro Phe Ala Thr Arg Asp Pro Lys  
1 5 10 15  
Ile Phe Asp Arg Ala Asp Glu Phe Val Pro Asp Arg Phe Thr Gly Glu  
20 25 30

<210> 30  
<211> 32  
<212> PRT  
<213> Cucumis melo

Gly Glu Leu Leu Cys Gly Tyr Gln Pro Phe Ala Thr Lys Asp Pro Lys

1 5 10 15  
Ile Phe Lys Asp Ser Glu Lys Phe Val Gly Asp Arg Phe Val Gly Glu  
20 25 30

&lt;212&gt; DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence:/Note =  
synthetic construct

agctaagtac	taattagttt	tatcatttac	agatagttaa	tctgtgtgat	cacggaagct	60
gtggcggagc	gcgcacacat	tattgagtat	tctgggttat	taaagtta	tcgttgtgat	120
cacgcaggtc	ttattttaat	gttgagatct	tctgtgtgtt	gtaacccacc	gggtcattta	180
tttttaagat	tgtttgtttt	ctcaaatatg	ctccaaattt	taaaataaat	aaataccatc	240
ttttcttttt	tactaaaaaa	aaaaaaataa	aa			270

<212> PRT

<213> Capsicum annum (green pepper)

Met Ile Pro Ile Met Ser Ser Ala Pro Leu Ser Thr Ala Thr Pro Ile

1                      5                      10                      15  
Ser Leu Pro Val Arg Lys Ile Pro Gly Ser Tyr Gly Phe Pro Leu Leu  
                        20                      25                      30

Gly Pro Leu Trp Asp Arg Leu Asp Tyr Asn Trp Phe Gln Lys Leu Pro  
35 40 45  
Asn Phe Phe Ser Lys Arg Val Glu Lys Tyr Asn Ser Thr Val Phe Arg

Asp	Phe	Phe	Ser	Lys	Arg	Val	Glu	Lys	Lys	Ala	Leu	Pro	Asn	Pro	Asn
50						55							60		
Thr	Asn	Val	Pro	Pro	Cys	Phe	Pro	Phe	Phe	Leu	Gly	Val	Asn	Pro	Asn
65					70					75					80

Val Val Ala Val Leu Asp Val Lys Ser Phe Ala His Leu Phe Asp Met  
85 90 95

Val Val Tyr Thr Gly Asp Met Arg Val Cys Ala Tyr Leu Asp Thr Ser

115 120 125  
Glu Pro Lys His Thr Gln Ile Lys Asn Phe Ser Leu Asp Ile Leu Lys  
130 135 140

Arg	Ser	Ser	Lys	Thr	Trp	Val	Pro	Thr	Leu	Val	Lys	Glu	Leu	Asp	Thr
145					150					155					160
Leu	Phe	Gly	Thr	Phe	Glu	Ser	Asp	Leu	Ser	Lys	Ser	Lys	Ser	Ala	Ser

Leu Leu Pro Ala Leu Gln Lys Phe Leu Phe Asn Phe Phe Ser Leu Thr  
165 170 175  
180 185 190

Phe Leu Gly Ala Asp Pro Ser Ala Ser Pro Glu Ile Ala Asn Ser Gly  
195 200 205  
Phe Ala Tyr Leu Asp Ala Trp Leu Ala Ile Gln Leu Ala Pro Thr Val

File	Alt	Ly	Med	NSP	Alt	HF	Med	Alt	---	---	---	---
210					215							220

Ser Ile Gly Val Leu Gln Pro Leu Glu Glu Ile Phe Val His Ser Phe  
 225 230 235 240  
 Ser Tyr Pro Tyr Phe Leu Val Arg Gly Gly Tyr Glu Lys Leu Ile Lys  
 245 250 255  
 Phe Val Lys Ser Glu Ala Lys Glu Val Leu Thr Arg Ala Gln Thr Asp  
 260 265 270  
 Phe Gln Leu Thr Glu Gln Glu Ala Ile His Asn Leu Leu Phe Ile Leu  
 275 280 285  
 Gly Phe Asn Ala Phe Gly Gly Phe Thr Ile Phe Leu Pro Thr Leu Leu  
 290 295 300  
 Gly Asn Leu Gly Asp Glu Lys Asn Ala Glu Met Gln Glu Lys Leu Arg  
 305 310 315 320  
 Lys Glu Val Arg Glu Lys Val Gly Thr Asn Gln Glu Asn Leu Ser Phe  
 325 330 335  
 Glu Ser Val Lys Glu Met Glu Leu Val Gln Ser Phe Val Tyr Glu Ser  
 340 345 350  
 Leu Arg Leu Ser Pro Pro Val Pro Ser Gln Tyr Ala Arg Ala Arg Lys  
 355 360 365  
 Asp Phe Met Leu Ser Ser His Asp Ser Val Tyr Glu Ile Lys Lys Gly  
 370 375 380  
 Glu Leu Leu Cys Gly Tyr Gln Pro Leu Val Met Lys Asp Pro Lys Val  
 385 390 395 400  
 Phe Asp Glu Pro Glu Lys Phe Met Leu Glu Arg Phe Thr Lys Glu Lys  
 405 410 415  
 Gly Lys Glu Leu Leu Asn Tyr Leu Phe Trp Ser Asn Gly Pro Gln Thr  
 420 425 430  
 Gly Ser Pro Thr Glu Ser Asn Lys Gln Cys Ala Ala Lys Asp Ala Val  
 435 440 445  
 Thr Leu Thr Ala Ser Leu Ile Val Ala Tyr Ile Phe Gln Lys Tyr Asp  
 450 455 460  
 Ser Val Ser Phe Ser Ser Gly Ser Leu Thr Ser Val Lys Lys Ala Cys  
 465 470 475 480

&lt;210&gt; 33

&lt;211&gt; 483

&lt;212&gt; PRT

&lt;213&gt; Banana

&lt;400&gt; 33

Met Ala Met Met Trp Ser Ser Ala Ser Ala Thr Ala Val Thr Thr Leu  
 1 5 10 15  
 Pro Thr Arg Pro Ile Pro Gly Ser Tyr Gly Pro Pro Leu Val Gly Pro  
 20 25 30  
 Leu Lys Asp Arg Leu Asp Tyr Phe Trp Phe Gln Gly Pro Glu Thr Phe  
 35 40 45  
 Phe Arg Ser Arg Met Ala Thr His Lys Ser Thr Val Phe Arg Thr Asn  
 50 55 60  
 Met Pro Pro Thr Phe Pro Phe Phe Val Gly Val Asp Pro Arg Val Val  
 65 70 75 80  
 Thr Val Leu Asp Cys Thr Ser Phe Ser Ala Leu Phe Asp Leu Glu Val  
 85 90 95  
 Val Glu Lys Lys Asn Ile Leu Ile Gly Asp Tyr Met Pro Ser Leu Ser  
 100 105 110  
 Phe Thr Gly Asp Thr Arg Val Val Val Tyr Leu Asp Pro Ser Glu Pro  
 115 120 125  
 Asp His Ala Arg Val Lys Ser Phe Cys Leu Glu Leu Leu Arg Arg Gly  
 130 135 140

Ala Lys Thr Trp Val Ser Ser Phe Leu Ser Asn Leu Asp Val Met Leu  
 145 150 155 160  
 Ala Thr Ile Glu Gln Gly Ile Ala Lys Asp Gly Ser Ala Gly Leu Phe  
 165 170 175  
 Gly Pro Leu Gln Lys Cys Ile Phe Ala Phe Leu Cys Lys Ser Ile Ile  
 180 185 190  
 Gly Ala Asp Pro Ser Val Ser Pro Asp Val Gly Glu Asn Gly Phe Val  
 195 200 205  
 Met Leu Asp Lys Trp Leu Ala Leu Gln Leu Leu Pro Thr Val Lys Val  
 210 215 220  
 Gly Ala Ile Pro Gln Pro Leu Glu Glu Ile Leu Leu His Ser Phe Pro  
 225 230 235 240  
 Leu Pro Phe Phe Leu Val Ser Arg Asp Tyr Arg Lys Leu Tyr Glu Phe  
 245 250 255  
 Val Glu Lys Gln Gly Gln Glu Val Val Arg Arg Ala Glu Thr Glu His  
 260 265 270  
 Gly Leu Ser Lys His Asp Ala Ile Asn Asn Ile Leu Phe Val Leu Gly  
 275 280 285  
 Phe Asn Ala Phe Gly Gly Phe Ser Val Phe Phe Pro Thr Leu Leu Thr  
 290 295 300  
 Thr Ile Gly Arg Asp Lys Thr Gly Leu Arg Glu Lys Leu Lys Asp Glu  
 305 310 315 320  
 Val Arg Arg Val Met Lys Ser Arg Gly Glu Lys Arg Pro Ser Phe Glu  
 325 330 335  
 Thr Val Arg Glu Met Glu Leu Val Arg Ser Thr Val Tyr Glu Val Leu  
 340 345 350  
 Arg Leu Asn Pro Pro Val Pro Leu Gln Tyr Gly Arg Ala Arg Thr Asp  
 355 360 365  
 Phe Thr Leu Asn Ser His Asp Ala Ala Phe Lys Val Glu Lys Gly Glu  
 370 375 380  
 Leu Leu Cys Gly Tyr Gln Pro Leu Val Met Arg Asp Pro Ala Val Phe  
 385 390 395 400  
 Asp Asp Pro Glu Thr Phe Ala Pro Glu Arg Phe Met Gly Ser Gly Lys  
 405 410 415  
 Glu Leu Leu Lys Tyr Val Phe Trp Ser Asn Gly Pro Glu Thr Gly Thr  
 420 425 430  
 Pro Thr Pro Ala Asn Lys Gln Cys Ala Ala Lys Asp Tyr Val Val Glu  
 435 440 445  
 Thr Ala Cys Leu Leu Met Ala Glu Ile Phe Tyr Arg Tyr Asp Glu Phe  
 450 455 460  
 Val Cys Ala Asp Asp Ala Ile Ser Val Thr Lys Leu Asp Arg Ala Arg  
 465 470 475 480  
 Glu Trp Glu

&lt;210&gt; 34

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&gt;220&gt;

 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

&lt;400&gt; 34

gggttatcagc cgctgggtgat g

<210> 35  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 35  
 atgaaccgga ggcgtttaat ccg

23

<210> 36  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 36  
 acagagcgga cgagttcgta cct

23

<210> 37  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 37  
 aggattcgga gaagttcgtg ggc

23

<210> 38  
 <211> 488  
 <212> PRT  
 <213> Psidium guava

<400> 38  
 Met Ala Arg Val Val Met Ser Asn Met Ser Pro Ala Met Ser Ser Thr  
 1 5 10 15  
 Tyr Pro Pro Ser Leu Ser Pro Pro Ser Ser Pro Arg Pro Thr Thr Leu  
 20 25 30  
 Pro Val Arg Thr Ile Pro Gly Ser Tyr Gly Trp Pro Leu Leu Gly Pro  
 35 40 45  
 Ile Ser Asp Arg Leu Asp Tyr Phe Trp Phe Gln Gly Pro Glu Thr Phe  
 50 55 60  
 Phe Arg Lys Arg Ile Glu Lys Tyr Lys Ser Thr Val Phe Arg Ala Asn  
 65 70 75 80  
 Val Pro Pro Cys Phe Pro Phe Phe Ser Asn Val Asn Pro Asn Val Val  
 85 90 95  
 Val Val Leu Asp Cys Glu Ser Phe Ala His Leu Phe Asp Met Glu Ile  
 100 105 110

Val Glu Lys Ser Asn Val Leu Val Gly Asp Phe Met Pro Ser Val Lys  
 115 120 125  
 Tyr Thr Gly Asn Ile Arg Val Cys Ala Tyr Leu Asp Thr Ser Glu Pro  
 130 135 140  
 Gln His Ala Gln Val Lys Asn Phe Ala Met Asp Ile Leu Lys Arg Ser  
 145 150 155 160  
 Ser Lys Val Trp Glu Ser Glu Val Ile Ser Asn Leu Asp Thr Met Trp  
 165 170 175  
 Asp Thr Ile Glu Ser Ser Leu Ala Lys Asp Gly Asn Ala Ser Val Ile  
 180 185 190  
 Phe Pro Leu Gln Lys Phe Leu Phe Asn Phe Leu Ser Lys Ser Ile Ile  
 195 200 205  
 Gly Ala Asp Pro Ala Ala Ser Pro Gln Val Ala Lys Ser Gly Tyr Ala  
 210 215 220  
 Met Leu Asp Arg Trp Leu Ala Leu Gln Leu Leu Pro Thr Ile Asn Ile  
 225 230 235 240  
 Gly Val Leu Gln Pro Leu Val Glu Ile Phe Leu His Ser Trp Ala Tyr  
 245 250 255  
 Pro Phe Ala Leu Val Ser Gly Asp Tyr Asn Lys Leu Tyr Gln Phe Ile  
 260 265 270  
 Glu Lys Glu Gly Arg Glu Ala Val Glu Arg Ala Lys Ala Glu Phe Gly  
 275 280 285  
 Leu Thr His Gln Glu Ala Ile His Asn Leu Leu Phe Ile Leu Gly Phe  
 290 295 300  
 Asn Ala Phe Gly Gly Phe Ser Ile Phe Leu Pro Thr Leu Leu Ser Asn  
 305 310 315 320  
 Ile Leu Ser Asp Thr Thr Gly Leu Gln Asp Arg Leu Arg Lys Glu Val  
 325 330 335  
 Arg Ala Lys Gly Gly Pro Ala Leu Ser Phe Ala Ser Val Lys Glu Met  
 340 345 350  
 Glu Leu Val Lys Ser Val Val Tyr Glu Thr Leu Arg Leu Asn Pro Pro  
 355 360 365  
 Val Pro Phe Gln Tyr Ala Arg Ala Arg Lys Asp Phe Gln Leu Lys Ser  
 370 375 380  
 His Asp Ser Val Phe Asp Val Lys Lys Gly Glu Leu Leu Cys Gly Tyr  
 385 390 395 400  
 Gln Lys Val Val Met Thr Asp Pro Lys Val Phe Asp Glu Pro Glu Ser  
 405 410 415  
 Phe Asn Ser Asp Arg Phe Val Gln Asn Ser Glu Leu Leu Asp Tyr Leu  
 420 425 430  
 Tyr Trp Ser Asn Gly Pro Gln Thr Gly Thr Pro Thr Glu Ser Asn Lys  
 435 440 445  
 Gln Cys Ala Ala Lys Asp Tyr Val Thr Leu Thr Ala Cys Leu Phe Val  
 450 455 460  
 Ala Tyr Met Phe Arg Arg Tyr Asn Ser Val Thr Gly Ser Ser Ser Ser  
 465 470 475 480  
 Ile Thr Ala Val Glu Lys Ala Asn  
 485

&lt;210&gt; 39

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:/Note =

## synthetic construct

<400> 39  
ccgtcagcac caccaaatcc ttc 23

<210> 40  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 40  
gaacagataa tccagcaggg c 21

<210> 41  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 41  
ctgaaccgac cgcgactgtg t 21

<210> 42  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 42  
tcgccgtga accgatcagg ta 22

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 43  
tcgcgctcgg ctccactgtc 20

<210> 44



<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 44  
tctcccacga acctatcgcc ca

22

<210> 45  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 45  
gccatggcct ccattgtcat tccttc

26

<210> 46  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 46  
ggaattcttta gtgatggatga tggatgatga aacttgcttt cttag

45

<210> 47  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 47  
gcataatggct actccttctt cctcctc

27

<210> 48  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 48  
catcgatttta gtgatgggtga tggatgatgat tagtcattag ctttaa 46

<210> 49  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 49  
atgaattcgg tacccgggat cctttttttt ttttttttt 39

<210> 50  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 50  
atgaattcgg tacccgggat c 21

<210> 51  
<211> 1596  
<212> DNA  
<213> Cucumis melo

<400> 51  
atgtcctcca ttgtcattcc ttctcttcaa cctcacttgc gattcccac ctcgcaagaa 60  
acgcctcaaa gatctcgttc tagagtggcg ttctgttcca tacgtccaat ctacgccacc 120  
gacggagttt ctctctcgto ttctctctct ctccaagtgc cgcagcggat tgtttcgccg 180  
cggaaccca ccaagcttcc tttagggaag gttcccggtg attatgggcc accgatgttt 240  
ggggcggtga aggacagaca tgattatttt tataatcagg ggagggaaaga gtatttgaaa 300  
ttcgaatgc tccggtatga atccactgtg tatagaacta atatgccgcc gggtccattt 360  
atcacttccg attcccgagt tgtgttttta ctgcacggga agagttttcc tgttcttttc 420  
gaccattcta aagttagaaa gaaagatctc ttatctggaa ctacatgcc tgtaacagag 480  
ctcaccggcg gttacagggg gctttcttat attgacccat ctgagcccca tcacgctaag 540  
ctcaaacagt tgatttttct ttctctcaa cccgcgggg ataaaaattt gccggaattt 600  
cactctaact ttctgtagct attcgagact ctggaaaagg atttggctgc tgctggtaga 660  
cgagagtaca atgcttccgg tgaacaagcg gcgtttaatt tcttggctgc gtctcttttc 720  
ggcgctgact cggtagatto caaattgggt cgcgatgcgc cgaatttgat cgcgaatagg 780  
gtcttattcc agcttggccc tgttctgagt ctggcctcc ccaaggtcgt cgaggagcct 840  
ctctctcgca cggctccggct ccccccggcg ttgattaaag ccgattaccg tccggtgtac 900  
gaacttcttt acaagtcgto ggagggcggtg tttagggagg cggatagatt ggggaatttcg 960  
agggagaag cttgtcaciaa cttgctattc acaacttgtt ttaattcatt tggagggatg 1020  
aagatctttt tccccaatat gataaaatgg atccggccag ccggagtgaa tctccacacc 1080  
cgactagcac gggagattcg tactgcgcta aaagcccaac gcgggaaaaa cacgatgggg 1140  
gctatggaac agatgcgcgt gatgaaatca gtggtgtacg aagcgtttaag aatcgagccg 1200  
ccggttccgg ttcatgacg tcgggcaaaag aaagaccttg tgggtggaaa ccacgacgcg 1260  
gtcttcgaga tcaaaagaag agaagtgatt tgtgggtatc agccattcgc aacaagagat 1320

cggaaaaatct	tcgacagagc	ggacgagttc	gtacctgac	ggttcacggg	cgagggtgag	1380
gagcttctca	aacacgtcat	atggtcaaac	ggaccggaaa	cacagtcgcc	gtcggttcag	1440
aacaagcagt	gcgcaggaaa	agacttcac	gtcttcac	ctcggcttct	cgctggtgaa	1500
ctttctctc	gttacgactc	cttcgacac	gaagctcaa	acactccgtt	aggtgccgcc	1560
gtcaccgtaa	cctccctaaa	gaaagcaagt	ttctaa			1596

&lt;210&gt; 52

&lt;211&gt; 465

&lt;212&gt; PRT

&lt;213&gt; Cucumis melo

&lt;400&gt; 52

Asn	Asp	Met	Ser	Ser	Ile	Val	Ile	Pro	Ser	Leu	Gln	Pro	His	Leu	Arg
1				5					10					15	
Phe	Pro	Ser	Ser	Gln	Glu	Thr	Pro	Gln	Arg	Ser	Arg	Ser	Arg	Val	Gly
			20					25					30		
Phe	Val	Ser	Ile	Arg	Pro	Ile	Tyr	Ala	Thr	Asp	Gly	Val	Ser	Ser	Ser
			35				40					45			
Ser	Ser	Ser	Ser	Leu	Gln	Val	Pro	Gln	Arg	Ile	Val	Ser	Pro	Pro	Glu
			50			55				60					
Pro	Thr	Lys	Leu	Pro	Leu	Arg	Lys	Val	Pro	Gly	Asp	Tyr	Gly	Pro	Pro
65					70					75				80	
Met	Phe	Gly	Ala	Leu	Lys	Asp	Arg	His	Asp	Tyr	Phe	Tyr	Asn	Gln	Gly
				85					90					95	
Arg	Glu	Glu	Tyr	Leu	Lys	Ser	Arg	Met	Leu	Arg	Tyr	Glu	Ser	Thr	Val
			100					105					110		
Tyr	Arg	Thr	Asn	Met	Pro	Pro	Gly	Pro	Phe	Ile	Thr	Ser	Asp	Ser	Arg
			115				120					125			
Val	Val	Val	Leu	Leu	Asp	Gly	Lys	Ser	Phe	Pro	Val	Leu	Phe	Asp	His
			130				135					140			
Ser	Lys	Val	Glu	Lys	Lys	Asp	Leu	Phe	Thr	Gly	Ala	Val	Phe	Glu	Glu
145					150					155				160	
Ala	Asp	Arg	Leu	Gly	Ile	Ser	Arg	Glu	Glu	Ala	Cys	His	Asn	Leu	Leu
				165						170				175	
Phe	Thr	Thr	Cys	Phe	Asn	Ser	Phe	Gly	Gly	Met	Lys	Ile	Phe	Phe	Pro
			180					185					190		
Asn	Met	Ile	Lys	Trp	Ile	Gly	Arg	Ala	Gly	Val	Asn	Leu	His	Thr	Arg
			195				200					205			
Leu	Ala	Arg	Glu	Ile	Arg	Thr	Ala	Val	Lys	Ala	Asn	Gly	Gly	Lys	Ile
			210				215					220			
Thr	Met	Gly	Ala	Met	Glu	Gln	Met	Pro	Leu	Met	Lys	Ser	Val	Val	Tyr
225					230					235				240	
Glu	Ala	Leu	Arg	Ile	Glu	Pro	Pro	Val	Pro	Val	Gln	Tyr	Gly	Arg	Ala
				245						250				255	
Lys	Lys	Asp	Leu	Val	Val	Glu	Ser	His	Asp	Ala	Ala	Phe	Glu	Ile	Lys
			260					265					270		
Glu	Gly	Glu	Val	Ile	Cys	Gly	Tyr	Gln	Pro	Phe	Ala	Thr	Arg	Asp	Pro
			275				280					285			
Lys	Ile	Phe	Asp	Arg	Ala	Asp	Glu	Leu	Val	Pro	Asp	Arg	Phe	Thr	Gly
			290			295					300				
Glu	Gly	Glu	Glu	Leu	Leu	Thr	Tyr	Met	Pro	Val	Thr	Glu	Leu	Thr	Gly
305					310					315				320	
Gly	Tyr	Arg	Val	Leu	Ser	Tyr	Ile	Asp	Pro	Ser	Glu	Pro	Asp	His	Ala
				325					330					335	
Lys	Leu	Lys	Gln	Leu	Ile	Phe	Phe	Leu	Leu	Lys	His	Arg	Arg	Asp	Lys
				340					345					350	

```

Ile Met Pro Glu Phe His Ser Thr Phe Ser Glu Leu Phe Glu Thr Leu
      355      360      365
Glu Lys Asp Leu Ala Ala Gly Arg Ala Glu Tyr Asn Ala Ser Gly
      370      375      380
Glu Gln Ala Ala Phe Asn Phe Leu Ala Arg Ser Leu Phe Gly Ala Asp
385      390      395      400
Pro Val Asp Ser Lys Leu Gly Arg Asp Ala Pro Lys Leu Ile Ala Lys
      405      410      415
Trp Val Leu Phe Gln Leu Gly Pro Val Leu Ser Leu Gly Leu Pro Lys
      420      425      430
Val Val Glu Glu Leu Leu Leu Arg Thr Val Arg Leu Pro Pro Ala Leu
      435      440      445
Ile Lys Ala Asp Tyr Arg Arg Leu Tyr Asp Phe Phe Tyr Lys Ser Ser
      450      455      460
Glu
465

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<210> 53
<211> 468
<212> PRT
<213> Flax

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<400> 53
Met Ala Ser Ser Ala Leu Asn Asn Leu Val Ala Val Asn Pro Asn Thr
1      5      10      15
Leu Ser Pro Ser Pro Lys Ser Thr Pro Leu Pro Asn Thr Phe Ser Asn
      20      25      30
Leu Arg Arg Val Ser Ala Phe Arg Pro Ile Lys Ala Ser Leu Phe Gly
      35      40      45
Asp Ser Pro Ile Lys Ile Pro Gly Ile Thr Ser Gln Pro Pro Pro Ser
50      55      60
Ser Asp Glu Thr Thr Leu Pro Ile Arg Gln Ile Pro Gly Asp Tyr Gly
65      70      75      80
Leu Pro Gly Ile Gly Pro Ile Gln Asp Arg Leu Asp Tyr Phe Tyr Asn
      85      90      95
Gln Gly Arg Glu Glu Phe Phe Lys Ser Arg Leu Gln Lys Tyr Lys Ser
      100      105      110
Thr Val Tyr Arg Ala Asn Met Pro Pro Gly Pro Phe Ile Ala Ser Asn
      115      120      125
Pro Arg Val Ile Val Leu Leu Asp Ala Lys Ser Phe Pro Val Leu Phe
130      135      140
Asp Met Ser Lys Val Glu Lys Lys Asp Leu Phe Thr Gly Ser Val Leu
145      150      155
Asp Glu Ala Glu Gln Ser Gly Ile Ser Arg Asp Glu Ala Cys His Asn
      165      170      175
Ile Leu Phe Ala Val Cys Phe Asn Ser Trp Gly Gly Phe Lys Ile Leu
      180      185      190
Phe Pro Ser Leu Met Lys Trp Ile Gly Arg Ala Gly Leu Glu Leu His
195      200      205
Thr Lys Leu Ala Gln Glu Ile Arg Ser Ala Ile Gln Ser Thr Gly Gly
210      215      220
Gly Lys Val Thr Met Ala Ala Met Glu Gln Met Pro Leu Met Lys Ser
225      230      235
Val Val Tyr Glu Thr Leu Arg Ile Glu Pro Pro Val Ala Leu Gln Tyr
      245      250      255
Gly Lys Ala Lys Lys Asp Phe Ile Leu Glu Ser His Glu Ala Tyr
260      265      270

```

Gln Val Lys Glu Gly Glu Met Leu Phe Gly Tyr Gln Pro Phe Ala Thr  
 275 280 285  
 Lys Asp Pro Lys Ile Phe Asp Arg Pro Glu Glu Phe Val Ala Asp Arg  
 290 295 300  
 Phe Val Gly Glu Gly Val Lys Leu Met Thr Tyr Met Pro Ser Thr Glu  
 305 310 315 320  
 Leu Thr Gly Gly Tyr Arg Ile Leu Ser Tyr Leu Asp Pro Ser Glu Pro  
 325 330 335  
 Asn His Thr Lys Leu Lys Gln Leu Leu Phe Asn Leu Ile Lys Asn Arg  
 340 345 350  
 Arg Asp Tyr Val Ile Pro Glu Phe Ser Ser Ser Phe Thr Asp Leu Cys  
 355 360 365  
 Glu Val Val Glu Tyr Asp Leu Ala Thr Lys Gly Lys Ala Ala Phe Asn  
 370 375 380  
 Asp Pro Ala Glu Gln Ala Ala Phe Asn Phe Leu Ser Arg Ala Phe Phe  
 385 390 395 400  
 Gly Val Lys Pro Ile Asp Thr Pro Leu Gly Lys Asp Ala Pro Ser Leu  
 405 410 415  
 Ile Ser Lys Trp Val Leu Phe Asn Leu Ala Pro Ile Leu Ser Val Gly  
 420 425 430  
 Leu Pro Lys Glu Val Glu Glu Ala Thr Leu His Ser Val Arg Leu Pro  
 435 440 445  
 Pro Leu Leu Val Gln Asn Asp Tyr His Arg Leu Tyr Glu Phe Phe Thr  
 450 455 460  
 Ser Ala Ala Gly  
 465

<210> 54  
 <211> 405  
 <212> PRT  
 <213> Guayule

<400> 54  
 Met Asp Pro Ser Ser Lys Pro Leu Arg Glu Ile Pro Gly Ser Tyr Gly  
 1 5 10 15  
 Ile Pro Phe Phe Gln Pro Ile Lys Asp Arg Leu Glu Tyr Phe Tyr Gly  
 20 25 30  
 Thr Gly Gly Arg Asp Glu Tyr Phe Arg Ser Arg Met Gln Lys Tyr Gln  
 35 40 45  
 Ser Thr Val Phe Arg Ala Asn Met Pro Pro Gly Pro Phe Val Ser Ser  
 50 55 60  
 Asn Pro Lys Val Ile Val Leu Leu Asp Ala Lys Ser Phe Pro Ile Leu  
 65 70 75 80  
 Phe Asp Val Ser Lys Val Glu Lys Lys Asp Leu Phe Thr Gly Pro Val  
 85 90 95  
 Met Glu Gln Ala Glu Lys Leu Gly Val Pro Lys Asp Glu Ala Val His  
 100 105 110  
 Asn Ile Leu Phe Ala Val Cys Phe Asn Thr Phe Gly Gly Val Lys Ile  
 115 120 125  
 Leu Phe Pro Asn Thr Leu Lys Trp Ile Gly Val Ala Gly Glu Asn Leu  
 130 135 140  
 His Thr Gln Leu Ala Glu Glu Ile Arg Gly Ala Ile Lys Ser Tyr Gly  
 145 150 155 160  
 Asp Gly Asn Val Thr Leu Glu Ala Ile Glu Gln Met Pro Leu Thr Lys  
 165 170 175  
 Ser Val Val Tyr Glu Ser Leu Arg Ile Glu Pro Pro Val Pro Gln  
 180 185 190

Tyr Gly Lys Ala Lys Ser Asn Phe Thr Ile Glu Ser His Asp Ala Thr  
 195 200 205  
 Phe Glu Val Lys Lys Gly Glu Met Leu Phe Gly Tyr Gln Pro Phe Ala  
 210 215 220  
 Thr Lys Asp Pro Lys Val Phe Asp Arg Pro Glu Glu Phe Val Pro Asp  
 225 230 235 240  
 Arg Phe Val Gly Asp Gly Glu Ala Leu Leu Thr Tyr Met Pro Ser Thr  
 245 250 255  
 Lys Leu Thr Gly Ala Tyr Arg Val Leu Ser Tyr Leu Asp Pro Ser Glu  
 260 265 270  
 Pro Arg His Ala Gln Leu Lys Asn Leu Leu Phe Phe Met Leu Lys Asn  
 275 280 285  
 Ser Ser Asn Arg Val Ile Pro Gln Phe Glu Thr Thr Tyr Thr Glu Leu  
 290 295 300  
 Phe Glu Gly Leu Glu Ala Glu Leu Ala Lys Asn Gly Lys Ala Ala Phe  
 305 310 315 320  
 Asn Asp Val Gly Glu Gln Ala Ala Phe Arg Phe Leu Gly Arg Ala Tyr  
 325 330 335  
 Phe Asn Ser Asn Pro Glu Glu Thr Lys Leu Gly Thr Ser Ala Pro Thr  
 340 345 350  
 Leu Ile Ser Ser Trp Val Leu Phe Asn Leu Ala Pro Thr Leu Asp Leu  
 355 360 365  
 Gly Leu Pro Trp Phe Leu Gln Glu Pro Leu Leu His Thr Phe Arg Leu  
 370 375 380  
 Pro Ala Phe Leu Ile Lys Ser Thr Tyr Asn Lys Leu Tyr Asp Tyr Phe  
 385 390 395 400  
 Gln Ser Val Ala Thr  
 405

&lt;210&gt; 55

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis

&lt;400&gt; 55

Met Ala Ser Ile Ser Thr Pro Phe Pro Ile Ser Leu His Pro Lys Thr  
 1 5 10 15  
 Val Arg Ser Lys Pro Leu Lys Phe Arg Val Leu Thr Arg Pro Ile Lys  
 20 25 30  
 Ala Ser Gly Ser Glu Thr Pro Asp Leu Thr Val Ala Thr Arg Thr Gly  
 35 40 45  
 Ser Lys Asp Leu Pro Ile Arg Asn Ile Pro Gly Asn Tyr Gly Leu Pro  
 50 55 60  
 Ile Val Gly Pro Ile Lys Asp Arg Trp Asp Tyr Phe Tyr Asp Gln Gly  
 65 70 75 80  
 Ala Glu Glu Phe Phe Lys Ser Arg Ile Arg Lys Tyr Asn Ser Thr Val  
 85 90 95  
 Tyr Arg Val Asn Met Pro Pro Gly Ala Phe Ile Ala Glu Asn Pro Gln  
 100 105 110  
 Val Val Ala Leu Leu Asp Gly Lys Ser Phe Pro Val Leu Phe Asp Val  
 115 120 125  
 Asp Lys Val Glu Lys Lys Asp Leu Phe Thr Gly Glu Ile Leu Val Glu  
 130 135 140  
 Ala Asp Lys Leu Gly Ile Ser Arg Glu Glu Ala Thr His Asn Leu Leu  
 145 150 155 160

Phe Ala Thr Ser Phe Asn Thr Trp Gly Gly Met Lys Ile Leu Phe Pro  
 165 170 175  
 Asn Met Val Lys Arg Ile Gly Pro Gly Gly His Gln Val His Asn Arg  
 180 185 190  
 Leu Ala Glu Glu Ile Arg Ser Val Ile Lys Ser Asn Gly Gly Glu Leu  
 195 200 205  
 Thr Met Gly Ala Ile Glu Lys Met Glu Leu Thr Lys Ser Val Val Tyr  
 210 215 220  
 Glu Cys Leu Arg Phe Glu Pro Pro Val Thr Ala Gln Tyr Gly Arg Ala  
 225 230 235 240  
 Lys Lys Asp Leu Val Ile Glu Ser His Asp Ala Ala Phe Lys Val Lys  
 245 250 255  
 Ala Gly Glu Met Leu Tyr Gly Tyr Gln Pro Leu Ala Thr Arg Asp Pro  
 260 265 270  
 Lys Ile Phe Asp Arg Ala Asp Glu Phe Val Pro Glu Arg Phe Val Gly  
 275 280 285  
 Glu Glu Gly Glu Lys Leu Leu Thr Tyr Met Pro Ser Thr Glu Leu Thr  
 290 295 300  
 Gly Gly Tyr Arg Ile Leu Ser Tyr Leu Asp Pro Ser Glu Pro Lys His  
 305 310 315 320  
 Glu Lys Leu Lys Asn Leu Leu Phe Phe Leu Leu Lys Ser Ser Asn Arg  
 325 330 335  
 Ile Phe Pro Glu Phe Gln Ala Thr Tyr Ser Glu Leu Phe Asp Ser Leu  
 340 345 350  
 Glu Lys Glu Ala Phe Pro Leu Arg Glu Ser Gly Phe Arg Arg Phe Gln  
 355 360 365  
 Arg Arg Asn Arg Leu Leu Phe Leu Gly Ser Ser Phe Leu Arg Asp Glu  
 370 375 380  
 Ser Arg Arg Tyr Lys Leu Lys Ala Asp Ala Pro Gly Leu Ile Thr Lys  
 385 390 395 400  
 Trp Val Leu Phe Asn Leu His Pro Leu Leu Ser Ile Gly Leu Pro Arg  
 405 410 415  
 Val Ile Glu Glu Pro Leu Ile His Thr Phe Ser Leu Pro Pro Ala Leu  
 420 425 430  
 Val Lys Ser Asp Tyr Gln Arg Leu Tyr Glu Phe Leu Arg Ile Arg Gly  
 435 440 445

&lt;210&gt; 56

&lt;211&gt; 1715

&lt;212&gt; DNA

&lt;213&gt; Cucumis melo

&lt;221&gt; misc\_feature

&lt;222&gt; 1283

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 56

atggctactc	ctttcttcctc	ctcccttgaa	cttctctctca	aaccaattcc	cggtggctat	60
ggcttccctc	tctctgggtcc	catcaaagac	cgttacgatt	acttctattt	ccaaggtaga	120
gacgaattct	tccgttcccg	gattaccaaa	tacaactoca	cgtctctccg	cgccaacatg	180
ccaccgggccc	cttctatttc	ctccgattcc	agagtcggtg	tccttctcga	tgccctcagt	240
tttctctatcc	ctttcgcacac	agcctaaagtc	gagaaaaagca	acattctcga	cggaaactac	300
atgcctctct	tgtccttcac	cggcaacatt	cgcacctgtg	cttatttggg	ccatcgagg	360
acagagcaact	ctgtttctcaa	acgcctcttc	ctctctcttc	tcgcttcccg	ccatgacagg	420
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